VL

D I Q M T Q T T S S L S A S L G D R V T gatatccagatgacccagactacatcctcctgtctgcctctctgggagacagagtcacc I S C R A S Q D I S N Y L N W Y Q Q K P attagttgcagggcaagtcaggacattagcaattatttaaactggtatcagcagaaacca D G T V K L L I Y Y T S I L H S G V P S gatggaactgttaaactcctgatctactacacatcaatattacactcaggagtcccatca R F S G S G S G T D Y S L T I S N L E Q aggttcagtggcagtgggtctggaacagattattctctcaccattagcaacctggagcaa E D F A T Y F C Q Q G N T L P W T F G G gaagattttgccactacttttgccaacagggtaatacgcttccgtggacgtcggtagaccaagctggaacacagctggaacacagctggaacacaagctggaaatcaaa

VH

E V Q L V E S G G G L V K P G G S L K L gaagtgcagctggagtctgggggagcttagtgaagcctggagggtccctgaaactc S C A A S G F A F S I Y D M S W V R Q T teetgtgcagcctctggattcgcttcagtatctatgacatgtcttgggttcgccagact P E K R L E W V A Y I S S G G G T T Y Y C c gaagaagaggctggagtggccatacattagtagtggtggtggtggtggtaccacctactat P D T V K G R F T I S R D N A K N T L Y ccagacactgtgaagggccgattcaccatctccagagacaatgccaagacaccctgtac L Q M S S L K S E D T A M Y Y C A R H S ctgcaaatggcagtctgaagtctgaggacacagccatgtattactgtgcaagacatagt G Y G S S Y G V L F A Y W G Q G T L V T gctacgfagtagccacgggtttgtttgtttgtttgcttactgggccaagggccact

. FIG. 1

Nucleotide/residue numbering shown first followed by Kabat Numbering

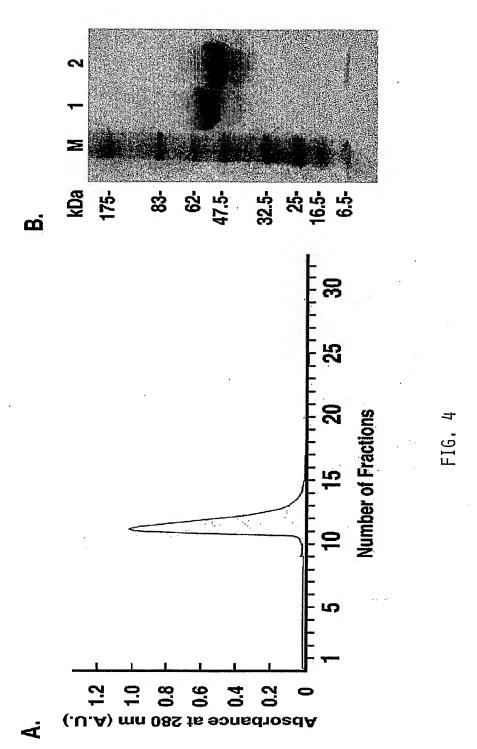
1	0	/ ^k			
2	1 gat ASP D	49	42 gga GLY G		
3	2 atc ILE I	50	43 act THR T	85	78 ctg LEU L
	_	51	44 gtt VAL V	86	79 gag GLU E
4	3 cag GLN Q	52	45 aaa LYS K	87	80 caa GLN Q
5	4 atg MET M	53	46 ctc LEU L	88	81 gaa GLU E
6	5 acc THR T	54	47 ctg LEU L	89	82 gat ASP D
7	6 cag GLN Q	55	48 atc ILE I	90	83 ttt PHE F
8	7 act THR T	56	49 tac TYR Y	91	84 gcc ALA A
9	8 aca THR T		50 tac TYR Y		
10	9 tcc SER S	57		92	85 act THR T
11	10 tcc SER S	5 8	51 aca THR T	93	86 tac TYR Y
12	11 ctg LEU L	59	52 tca SER S	94	87 ttt PHE F
13	12 tot SER S	60	53 ata ILE I	95	88 tgc CYS C
14	13 gcc ALA A	61	54 tta LEU L	96	89 caa GLN Q
15	14 tot SER S	62	55 cac HIS H	97	90 cag GLN Q
16		63	56 tca SER S	98	91 ggt GLY G
10	15 ctg LEU L	64	57 gga GLY G	· 9 9	92 aat ASN N
	*	65	58 gtc VAL V	100	93 acg THR T
17	16 can GIV C	66	59 cca PRO P	101	94 ctt LEU L
17	16 gga GLY G	67	60 tca SER S	102	95 ccg PRO P
18	17 gac ASP D	68	61 agg ARG R	103	95A
19	18 aga ARG R		62 ttc PHE F		95B
20	19 gtc VAL V	69 70		104	
21	20 acc THR T	70	63 agt SER S	105	95C
22	21 att ILE I	71	64 ggc GLY G	1 06 [.]	95D
23	22 agt SER S	72	65 agt SER S	107	95E
24	23 tgc CYS C	73	66 ggg GLY G	108	95F
25	24 agg ARG R	74	67 tct SER S	109	96 tgg TRP W
26	25 gca ALA A	75 `	68 gga GLY G	110	97 acg THR T
27	26 agt SER S	76	69 aca THR T	111	98 ttc PHE F
28	27 cag GLN Q	77	70 gat ASP D	112	99 ggt GLY G
29	27A	78	71 tat TYR Y	113	100 gga GLY G
	27B	79	72 tct SER S	114	101 ggc GLY G
30		80	73 ctc LEU L	115	102 acc THR T
31	27C	81	74 acc THR T	116	103 aag LYS K
32	27D	82	75 att ILE I		104 ctg LEU L
33	27E	83	76 age SER S	117	
34	27F			118	105 gaa GLU E
35	28 gac ASP D	8.4	77 aac ASN N	119	106 atc ILE I
36	29 att ILE I			120	106A
37	30 agc SER S			121	107 aaa LYS K
38	31 aat ASN N			122	108
39	32 tat TYR Y			. 123	109 •
40	33 tta LEU L				
41	34 aac ASN N		•		
42	35 tgg TRP W				
43	36 tat TYR Y				
44	37 cag GLN Q				
45	38 cag GLN Q				
46	39 aaa LYS K				
47	40 cca PRO P				
48	41 gat ASP D				

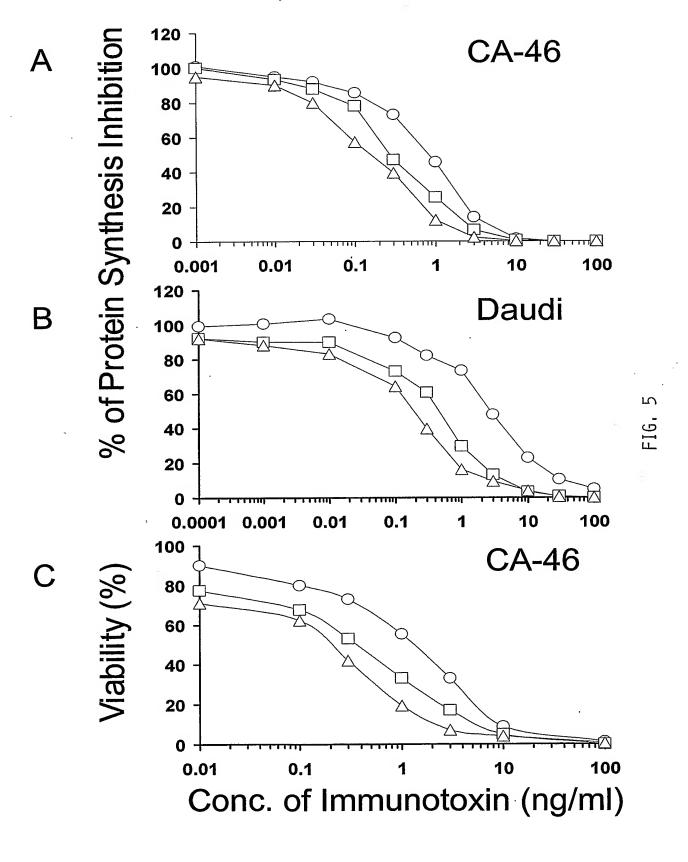
FIG. 2

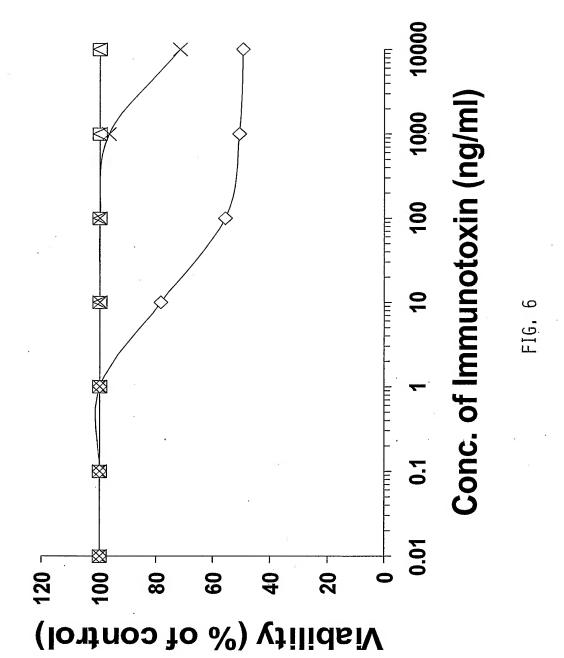
Nucleotide/residue numbering shown first followed by Kabat Numbering

	_	49	46 gag GLU E		
1	0	50	47 tgg TRP W	85	79 tac TYR Y
2	1 gaa GLU E	51	48 gtc VAL V	86	80 ctg LEU L
3	2 gtg VAL V	52	49 gca ALA A	87	81 caa GLN Q
4	3 cag GLN Q	53	50 tac TYR Y	88	82 atg MET M
5	4 ctg LEU L			89	82A agc SER S
6	5 gtg VAL V	54 ,	51 att ILE I	90	_
7	6 gag GLU E	55	52 agt SER S		82B agt SER S
		56	52A agt SER S	91	82C ctg LEU L
8	7 tot SER S	57	52B	92	83 aag LYS K
9	8 ggg GLY G	58	52C	93	84 tot SER S
10	9 gga GLY G	59	53 ggt GLY G	94	85 gag GLU E
11	10 ggc GLY G	60	54 ggt GLY G	95	86 gac ASP D
12	11 tta LEU L	61	55 ggt GLY G	96	87 aca THR T
13	12 gtg VAL V	62	56 acc THR T	97	88 gcc ALA A
14	13 aag LYS K		57 acc THR T	98	89 atg MET M
15	14 cct PRO P	63		99	90 tat TYR Y
16	15 gga GLY G	64	58 tac TYR Y	100	91 tac TYR Y
	35 ·	65	59 tat TYR Y		
17	16 ggg GLY G	66	60 cca PRO P	101	92 tgt CYS C
18	17 tcc SER S	67	61 gac ASP D	102	93 gca ALA A
19	18 ctg LEU L	68	62 act THR T	103	94 aga ARG R
20	19 aaa LYS K	69	63 gtg VAL V	104	95 cat HIS H
	20 ctc LEU L	70	64 aag LYS K	105	96 agt SER S
21	21 tcc SER S	71	65 ggc GLY G	106	97 ggc GLY G
22		72	66 cga ARG R	107	98 tac TYR Y
23	22 tgt CYS C	73	67 ttc PHE F	108	99 ggt GLY G
24	23 gca ALA A		68 acc THR T	109	100 agt SER S
25	24 gcc ALA A	74		110	100A agc SER S
26	25 tet SER S	75	69 atc ILE I	111	100B tac TYR Y
27	26 gga GLY G	76	70 tcc SER S		
28	27 ttc PHE F	77	71 aga ARG R	112	100C ggg GLY G
29	28 gct ALA A	7 8	72 gac ASP D	113	100D gtt VAL V
30	29 ttc PHE F	79	73 aat ASN N	114	100E ttg LEU L
31	30 agt SER S	80	74 gcc ALA A	115	100F
	31 atc ILE I	81	75 aag LYS K	116	100G
32	32 tat TYR Y	82	76 aac ASN N	117	100H
33		83		118	1001
34	33 gac ASP D	84	78 ctg LEU L	119	100J
35	34 atg MET M	0.4	70 CCg 22C 2	120	100K ttt PHE F
36	35 tot SER S			121	101 gct ALA A
37	35A			122	102 tac TYR Y
38	35B			123	103 tgg TRP W
39	36 tgg TRP W				
40	37 gtt VAL V			124	
41	38 cgc ARG R			125	105 caa GLN Q
42	39 cag GLN Q			126	106 ggg GLY G
43	40 act THR T			127	107 act THR T
44	41 ccg PRO P			12 8	108 ctg LEU L
45	42 gag GLU E			129	109 gtc VAL V
	42 gag GHO H 43 aag LYS K			130	110 act THR T
46	45 aay Die N			131	111 gtc VAL V
47	44 agg ARG R			132	112 tct SER S
48	45 ctg LEU L			133	113 gca ALA A

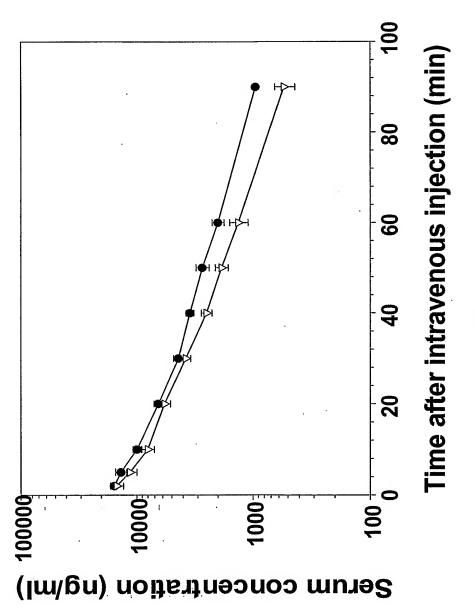
FIG. 3







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